

## **Genetic diversity of recent infectious bursal disease viruses isolated from vaccinated poultry flocks in Malaysia**

### **ABSTRACT**

Vaccination is an essential component in controlling infectious bursal disease (IBD), however, there is a lack of information on the genetic characteristics of a recent infectious bursal disease virus (IBDV) that was isolated from IBD vaccinated commercial flocks in Malaysia. The present study investigated 11 IBDV isolates that were isolated from commercial poultry farms. The isolates were detected using reverse transcription-polymerase chain reaction (RT-PCR) targeting the hypervariable region (HVR) of VP2. Based on the HVR sequences, five isolates (IBS536/2017, IBS624/2017, UPM766/2018, UPM1056/2018, and UPM1432/2019) were selected for whole-genome sequencing using the MiSeq platform. The nucleotide and amino acid (aa) sequences were compared with the previously characterized IBDV strains. Deduced aa sequences of VP2HVR revealed seven isolates with 94-99% aa identity to very virulent strains (genogroup 3), two isolates with 97-100% aa identity to variant strains (genogroup 2), and two strains with 100% identity to the vaccine strain (genogroup 1) of IBDV. The phylogenetic analysis also showed that the isolates formed clusters with the respective genogroups. The characteristic motifs 222T, 249K, 286I, and 318D are typical of the variant strain and were observed for UPM1219/2019 and UPM1432/2019. In comparison, very virulent residues such as 222A, 249Q, 286T, and 318G were found for the vvIBDV, except for the UPM1056/2018 strain with a A222T substitution. In addition, the isolate has aa substitutions such as D213N, G254D, S315T, S317R, and A321E that are not commonly found in previously reported vvIBDV strains. Unlike the other vvIBDVs characterized in this study, UPM766/2018 lacks the MLSL aa residues in VP5. The aa tripeptides 145/146/147 (TDN) of VP1 were conserved for the vvIBDV, while a different motif, NED, was observed for the Malaysian variant strain. The phylogenetic tree showed that the IBDV variant clustered with the American and Chinese variant viruses and are highly comparable to the novel Chinese variants, with 99.9% identity. Based on the sequences and phylogenetic analyses, this is the first identification of an IBDV variant being reported in Malaysia. Further research is required to determine the pathogenicity of the IBDV variant and the protective efficacy of the current IBD vaccines being used against the virus.

**Keyword:** Chickens; Infectious bursal disease virus; Next-generation sequencing; Variant IBDV; vvIBDV